



SEQUENCE LISTING

<110> Goedegebuur, Frits  
Gualfetti, Peter  
Mitchinson, Colin  
Neefe, Paulien

<120> Novel CBH1 Homologs and Variant CBH1  
Cellulases

<130> GC793-3

<140> US 10/804,785

<141> 2004-03-19

<150> US 60/456,368

<151> 2003-03-21

<150> US 60/458,696

<151> 3003-03-27

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1491

<212> DNA

<213> Hypocrea jecorina

<400> 1

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acgtacggag	ttaccacacg	cggtaacacgc	ctctccattg	gctttgtcac	ccagtctgcg	300
cagaagaacg	ttggcgctcg	ccttacctt	atggcgagcg	acacgaccta	ccaggaattc	360
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atctccgagg	ctcttacccc	ccacccttgc	acgactgtcg	gccaggagat	ctgcgagggt	720
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tactctggca	acgagctcaa	cgttattac	tgcacagctg	aggaggcaga	attcggcgga	1020
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aaccctgctg	gcaccaccc	cacccggcc	ccagccacta	ccacttggaa	ctctcccgga	1380
cctaccctgt	ctcaactacgg	ccagtgccgc	ggtattggct	acagcgcccc	cacggctctgc	1440
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<210> 2

<211> 497

<212> PRT

<213> Hypocrea jecorina

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 20 25 30  
 Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr  
 35 40 45  
 Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn  
 50 55 60  
 Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser  
 65 70 75 80  
 Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val  
 85 90 95  
 Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala  
 100 105 110  
 Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser  
 115 120 125  
 Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu  
 130 135 140  
 Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr  
 145 150 155 160  
 Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys  
 165 170 175  
 Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp  
 180 185 190  
 Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser  
 195 200 205  
 Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala  
 210 215 220  
 Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly  
 225 230 235 240  
 Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys  
 245 250 255  
 Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser  
 260 265 270  
 Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu  
 275 280 285  
 Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr  
 290 295 300  
 Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser  
 305 310 315 320  
 Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala  
 325 330 335  
 Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe  
 340 345 350  
 Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp  
 355 360 365  
 Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn  
 370 375 380  
 Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser  
 385 390 395 400  
 Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val  
 405 410 415  
 Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro  
 420 425 430  
 Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr  
 435 440 445  
 Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser  
 450 455 460  
 His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys  
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Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys  
 485 490 495  
 Leu

<210> 3  
 <211> 1635  
 <212> DNA  
 <213> Hypocrea orientalis

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 aggctccgtg gtcatcgacg ccaactggcg ctggactcac gcgactaaca gcagcacgaa 180  
 ctgctacgac ggcacacactt ggagctcaac cctatgcctt gacaacgaga cttgcgcgaa 240  
 gaattgtcgc ctggacgggtg ccgccttatgc gtccacgtac ggagtcacca cgagtgccga 300  
 cagcctctcc atcggcttcg tcacgcaatc tgcacagaaag aacgttggcg cccgtctcta 360  
 cctgtatggcg agtgacacga cttaccagga gttcacgctg cttggcaacg agttctcttt 420  
 tgacgttgcat gtttcgcagc tgccgttaagt gacaaccatt ccccgcgagg ccatcttctc 480  
 attgggttccg agctgacccg ccgatctaag atgtggctt aacggcgctc tgcgttgcgt 540  
 gtctatggat gcccgttgcgt ggcgtgagcaa gtatcccacc aacaccgcgc ggcacaagta 600  
 cggcacgggc tactgacgaca gccagtgccc ccgcgtatctc aagttcatca acggccaggc 660  
 caacgttgcac ggctgggagc cgtccctccaa caacgcacac acgggtattt ggcggacacgg 720  
 aagctgctgc tctgagatgg atatctgggaa ggcacactcc atctccgagg ctctgactcc 780  
 tcacccttgc acgactgttg gccagagat ctgcacgtt gacggctgcg ggcggacacta 840  
 ctccaaacgac cgatatgggt gtaacttgcga tcctgtatgt tgcgttgcgaa atccataccg 900  
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 cccggcaccac caccaccgcg cggccagcta ccaccactgg aagctctccc ggacctactc 1560  
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 gcacgacactg ccagg 1635

<210> 4  
 <211> 17  
 <212> PRT  
 <213> Hypocrea orientalis

<400> 4  
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 1 5 10 15  
 Ala

<210> 5  
 <211> 497  
 <212> PRT  
 <213> Hypocrea orientalis

<400> 5  
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 20 25 30  
 Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr

35	40	45	
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn			
50	55	60	
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser			
65	70	75	80
Thr Tyr Gly Val Thr Thr Ser Ala Asp Ser Leu Ser Ile Gly Phe Val			
85	90	95	
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala			
100	105	110	
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser			
115	120	125	
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu			
130	135	140	
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr			
145	150	155	160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys			
165	170	175	
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp			
180	185	190	
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser			
195	200	205	
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala			
210	215	220	
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Asp Gly			
225	230	235	240
Asp Gly Cys Gly Gly Thr Tyr Ser Asn Asp Arg Tyr Gly Gly Thr Cys			
245	250	255	
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser			
260	265	270	
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu			
275	280	285	
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr			
290	295	300	
Val Gln Asn Gly Val Thr Tyr Gln Gln Pro Asn Ala Glu Leu Gly Ser			
305	310	315	320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ser			
325	330	335	
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe			
340	345	350	
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp			
355	360	365	
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn			
370	375	380	
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser			
385	390	395	400
Ser Gly Val Pro Ala Gln Leu Glu Ser Gln Ser Pro Asn Ala Lys Val			
405	410	415	
Val Tyr Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro			
420	425	430	
Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr			
435	440	445	
Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Thr			
450	455	460	
His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys			
465	470	475	480
Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys			
485	490	495	
Leu			

<210> 6  
<211> 1589

<212> DNA

<213> Hypocre a schweintzii

<400> 6

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gttgtgattt	gaatccatac	cgcttggca	acaccagctt	ctatggccct	ggctcgagct	900
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tcaaccgtta	ctatgtccag	aatggcgtca	cttaccagca	acccaacgccc	gagctcgca	1020
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<210> 7

<211> 17

<212> PRT

<213> Hypocre a schweintzii

<400> 7

Met	Tyr	Arg	Lys	Leu	Ala	Val	Ile	Thr	Ala	Phe	Leu	Ala	Thr	Ala	Arg
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Ala															

<210> 8

<211> 497

<212> PRT

<213> Hypocre a schweintzii

<400> 8

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Gln	Lys	Cys	Ser	Ser	Gly	Gly	Thr	Cys	Thr	Gln	Gln	Thr	Gly	Ser	Val
	20				25				30						
Val	Ile	Asp	Ala	Asn	Trp	Arg	Trp	Thr	His	Ala	Thr	Asn	Ser	Ser	Thr
	35				40				45						
Asn	Cys	Tyr	Asp	Gly	Asn	Thr	Trp	Ser	Ser	Thr	Leu	Cys	Pro	Asp	Asn
	50				55				60						
Glu	Thr	Cys	Ala	Lys	Asn	Cys	Cys	Leu	Asp	Gly	Ala	Ala	Tyr	Ala	Ser
	65				70				75				80		
Thr	Tyr	Gly	Val	Thr	Thr	Ser	Ala	Asp	Ser	Leu	Ser	Ile	Gly	Phe	Val
				85				90				95			
Thr	Gln	Ser	Ala	Gln	Lys	Asn	Val	Gly	Ala	Arg	Leu	Tyr	Leu	Met	Ala

100	105	110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser		
115	120	125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu		
130	135	140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr		
145	150	155
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys		
165	170	175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp		
180	185	190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser		
195	200	205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala		
210	215	220
Leu Thr Pro His Pro Cys Thr Asn Val Gly Gln Glu Ile Cys Asp Gly		
225	230	235
Asp Gly Cys Gly Gly Thr Tyr Ser Asn Asp Arg Tyr Gly Gly Thr Cys		
245	250	255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser		
260	265	270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu		
275	280	285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr		
290	295	300
Val Gln Asn Gly Val Thr Tyr Gln Gln Pro Asn Ala Glu Leu Gly Ser		
305	310	315
Tyr Ser Gly Asn Glu Leu Asn Asp Ala Tyr Cys Thr Ala Glu Glu Ser		
325	330	335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe		
340	345	350
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp		
355	360	365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn		
370	375	380
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser		
385	390	395
Ser Gly Val Pro Ala Gln Leu Glu Ser Gln Ser Ala Asn Ala Lys Val		
405	410	415
Val Tyr Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro		
420	425	430
Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr		
435	440	445
Arg Arg Pro Ala Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Thr		
450	455	460
His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Ile Cys		
465	470	475
Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys		
485	490	495
Leu		

<210> 9  
 <211> 1588  
 <212> DNA  
 <213> Trichoderma konilangbra

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 cacgcgacta acagcaccac gaactgctac gacggtaaca cttggagctc cagtcttgc 180  
 cccgacaatg agagttgcgc aaagaactgc tgcctggacg gtgcagccta cgcacccacg 240

tacggagtca	ccacgagtgc	tgatagcctc	tccattggct	tcgtcactca	gtctcagcag	300
aagaatgttgcg	ctcgatctc	ctacctgatg	gcaagcgaca	cgacctacca	ggaatttacc	360
ctgcttggca	acgagttctc	tttcgatgtt	gatgtttcac	agctgccgt	agtgactagc	420
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aacactgccc	gcccggcaagta	cggcacgggc	tactgcgata	gccagtgtcc	ccgtgatttg	600
aagttcatca	acggcgaggc	caacgttgc	ggctgggagc	cggcttcgaa	caacgccaac	660
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atctctgagg	cccttactcc	tcacccttgc	acgactgtcg	gccaggccat	ttgcgatgg	780
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aaccgatact	atgtccagaa	tggcgtca	ttccagcagc	ccaacgcccga	gctcggtagc	1020
tactctggca	acacgctca	cgatgttac	tgcgagctg	aagaggcgg	attcggcgga	1080
tcatctttct	cagacaagg	tggccttacc	caattcaagc	aggctacttc	aggcggcatg	1140
gtcttgggta	tgagcctgt	ggatgacgt	agttcatgga	tagattgac	attgtcgaga	1200
gaaccatagc	cgctgaccga	gacacaacag	tactacgcca	acatgctgt	gctggactcc	1260
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aacatcaagt	tcggaccat	tggcagact	gttaactcca	gcggcgaaa	ccccccggc	1440
ggagggaaacc	ccccccggc	caccacc	cgacgcccag	ctaccacc	cggaagctct	1500
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<210> 10

<211> 17

<212> PRT

<213> Trichoderma konilangbra

<400> 10

Met	Tyr	Arg	Lys	Leu	Ala	Val	Ile	Thr	Ala	Phe	Leu	Ala	Thr	Ala	Arg
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Ala															

<210> 11

<211> 498

<212> PRT

<213> Trichoderma konilangbra

<220>

<221> VARIANT

<222> 273

<223> Xaa = Any Amino Acid

<400> 11

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Gln	Lys	Cys	Ser	Ser	Gly	Gly	Ser	Cys	Thr	Ser	Gln	Thr	Gly	Ser	Val
								20			25		30		
Val	Ile	Asp	Ala	Asn	Trp	Arg	Trp	Thr	His	Ala	Thr	Asn	Ser	Thr	Thr
								35			40		45		
Asn	Cys	Tyr	Asp	Gly	Asn	Thr	Trp	Ser	Ser	Leu	Cys	Pro	Asp	Asn	
								50			55		60		
Glu	Ser	Cys	Ala	Lys	Asn	Cys	Cys	Leu	Asp	Gly	Ala	Ala	Tyr	Ala	Ser
								65			70		75		80
Thr	Tyr	Gly	Val	Thr	Thr	Ser	Ala	Asp	Ser	Leu	Ser	Ile	Gly	Phe	Val
								85			90		95		
Thr	Gln	Ser	Gln	Gln	Lys	Asn	Val	Gly	Ala	Arg	Leu	Tyr	Leu	Met	Ala
								100			105		110		
Ser	Asp	Thr	Thr	Tyr	Gln	Glu	Phe	Thr	Leu	Leu	Gly	Asn	Glu	Phe	Ser
								115			120		125		

Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu  
 130 135 140  
 Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Ser  
 145 150 155 160  
 Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys  
 165 170 175  
 Pro Arg Asp Leu Lys Phe Ile Asn Gly Glu Ala Asn Val Glu Gly Trp  
 180 185 190  
 Glu Pro Ala Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser  
 195 200 205  
 Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala  
 210 215 220  
 Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Ala Ile Cys Asp Gly  
 225 230 235 240  
 Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asp Arg Tyr Gly Gly Thr Cys  
 245 250 255  
 Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser  
 260 265 270  
 Xaa Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Met  
 275 280 285  
 Thr Val Val Thr Gln Phe Ala Thr Ser Gly Ala Ile Asn Arg Tyr Tyr  
 290 295 300  
 Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser  
 305 310 315 320  
 Tyr Ser Gly Asn Thr Leu Asn Asp Ala Tyr Cys Ala Ala Glu Glu Ala  
 325 330 335  
 Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe  
 340 345 350  
 Lys Gln Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp  
 355 360 365  
 Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Ile Tyr Pro Thr Asn  
 370 375 380  
 Glu Thr Ser Ser Thr Pro Gly Ala Ala Arg Gly Ser Cys Ser Thr Ser  
 385 390 395 400  
 Ser Gly Val Pro Ala Gln Leu Glu Ser Gln Ser Thr Asn Ala Lys Val  
 405 410 415  
 Val Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Ser  
 420 425 430  
 Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr  
 435 440 445  
 Thr Arg Arg Pro Ala Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln  
 450 455 460  
 Thr His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val  
 465 470 475 480  
 Cys Ala Ser Gly Ser Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln  
 485 490 495  
 Cys Leu

<210> 12  
 <211> 1592  
 <212> DNA  
 <213> Trichoderma pseudokoningii

<400> 12  
 tcggcctgca ccctccagac ggaaactcac ccgcctctga catggcagaa atgctcatct 60  
 ggtggcaatt gcacccaaca gacgggctcc gtggtcatcg acgcgaactg gcgctggact 120  
 cacgctacga acagcagcac gaactgctac gacggtaaca cttggagctc aaccttgc 180  
 cctgacaatg agacttgcgc gaagaactgc tgcttggatg gtgcgccta cgcgtcgacg 240  
 tacggagtca ccacgagcgc tgacagcctc tccattggct tcgtcactca gtctgcgcag 300  
 aagaatgtcg gcgcccgtct ctacttgatg gcgagtgaca cgacctacca agaatttacc 360  
 ctgcttggca acgagttctc cttcgatgtt gatgtttccc agctgccgta agtggccaa 420

tacaccctt	gacggtatcc	tctcattgg	tcccagctga	ctcgcaaat	taagatgtgg	480
cttgaacgga	gctctttact	tcgtgtccat	gacgcggat	ggtggcgtga	gcaagtatcc	540
cacaacact	gccggcgcca	agtacggcac	gggttactgt	gacagccagt	gccctcgta	600
tctcaagttc	atcaacggcg	aggccaacgt	tgagggctgg	gagccgttct	ccaacaacgc	660
caacacgggc	attggcggac	atggaagctg	ctgctctgag	atggatatct	gggaggccaa	720
ctccatctct	gaggcttta	ctcctcatcc	ttgcacgacc	gtcgggcagg	aaatttgcga	780
tggtgactcc	tgccggaa	cctactccgg	tgatcgat	ggcggtaactt	gcgatcctga	840
tggctcgat	tggAACCCat	accgcttggg	caacaccaggc	ttctacgggc	ccggctcaag	900
tttcgctctt	gataccacca	agaagttgac	cgttgtcacc	cagttcgaga	ttcgggcgc	960
tatcaaccgg	tactacgtcc	agaatggcgt	cactttccag	cagcccaacg	ccgagctcgg	1020
tagttactct	ggcaactcgc	tcgacgatga	ctactgcgcg	gctgaagagg	cggagtttgg	1080
tggctcttct	tttcgacaa	agggccgcct	tactcaattc	aaaaaggcta	ttccgggtgg	1140
catggctttg	gtcatgagct	tgtggatga	tgtgagttca	tgaatagcat	tcaaacagtc	1200
aacagaataa	cagcagctga	ctgagacaca	atagtactac	gccaacatgc	tgtggctgga	1260
ctccacccat	ccgacgaacg	agaccttcc	caccccccgt	gccgtgcgcg	gaagctgctc	1320
caccagctcc	ggtgtccctg	ctcagcttga	gtcccagct	tccaacgcca	aggtcgtata	1380
ctccaacatc	aagttcggcc	ctatccgcag	cacccggcaac	tccagcggcg	gtagccctcc	1440
cggcggagga	aaccctcccg	gtaccacgac	cacccggccgc	ccagctacct	ccactgaaag	1500
ctctcccgcc	cctactcaga	cgcactatgg	ccagtcgggt	ggtattgggt	actcgggccc	1560
cacggctctgc	gcgagtgcc	gcacttgcc	gg			1592

<210> 13

<211> 17

<212> PRT

<213> Trichoderma pseudokoningii

<400> 13

Met	Tyr	Arg	Lys	Leu	Ala	Val	Ile	Thr	Ala	Phe	Leu	Ala	Thr	Ala	Arg
1				5					10				15		
Ala															

<210> 14

<211> 498

<212> PRT

<213> Trichoderma pseudokoningii

<400> 14

Gln	Ser	Ala	Cys	Thr	Leu	Gln	Thr	Glu	Thr	His	Pro	Pro	Leu	Thr	Trp
1					5			10					15		
Gln	Lys	Cys	Ser	Ser	Gly	Gly	Thr	Cys	Thr	Gln	Gln	Thr	Gly	Ser	Val
								20				25			30
Val	Ile	Asp	Ala	Asn	Trp	Arg	Trp	Thr	His	Ala	Thr	Asn	Ser	Ser	Thr
								35			40			45	
Asn	Cys	Tyr	Asp	Gly	Asn	Thr	Trp	Ser	Ser	Thr	Leu	Cys	Pro	Asp	Asn
					50			55			60				
Glu	Thr	Cys	Ala	Lys	Asn	Cys	Cys	Leu	Asp	Gly	Ala	Ala	Tyr	Ala	Ser
								65			70		75		80
Thr	Tyr	Gly	Val	Thr	Thr	Ser	Ala	Asp	Ser	Leu	Ser	Ile	Gly	Phe	Val
								85			90			95	
Thr	Gln	Ser	Ala	Gln	Lys	Asn	Val	Gly	Ala	Arg	Leu	Tyr	Leu	Met	Ala
								100			105			110	
Ser	Asp	Thr	Thr	Tyr	Gln	Glu	Phe	Thr	Leu	Leu	Gly	Asn	Glu	Phe	Ser
								115			120			125	
Phe	Asp	Val	Asp	Val	Ser	Gln	Leu	Pro	Cys	Gly	Leu	Asn	Gly	Ala	Leu
								130			135			140	
Tyr	Phe	Val	Ser	Met	Asp	Ala	Asp	Gly	Gly	Val	Ser	Lys	Tyr	Pro	Thr
								145			150			155	
Asn	Thr	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ser	Gln	Cys
								165			170			175	
Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Glu	Ala	Asn	Val	Glu	Gly	Trp
								180			185			190	

Glu Pro Phe Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser  
 195 200 205  
 Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala  
 210 215 220  
 Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Asp Gly  
 225 230 235 240  
 Asp Ser Cys Gly Gly Thr Tyr Ser Gly Asp Arg Tyr Gly Gly Thr Cys  
 245 250 255  
 Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser  
 260 265 270  
 Phe Tyr Gly Pro Gly Ser Ser Phe Ala Leu Asp Thr Thr Lys Lys Leu  
 275 280 285  
 Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr  
 290 295 300  
 Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser  
 305 310 315 320  
 Tyr Ser Gly Asn Ser Leu Asp Asp Asp Tyr Cys Ala Ala Glu Glu Ala  
 325 330 335  
 Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe  
 340 345 350  
 Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp  
 355 360 365  
 Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn  
 370 375 380  
 Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser  
 385 390 395 400  
 Ser Gly Val Pro Ala Gln Leu Glu Ser Gln Ser Ser Asn Ala Lys Val  
 405 410 415  
 Val Tyr Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Ser  
 420 425 430  
 Ser Gly Gly Ser Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr  
 435 440 445  
 Thr Arg Arg Pro Ala Thr Ser Thr Gly Ser Ser Pro Gly Pro Thr Gln  
 450 455 460  
 Thr His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val  
 465 470 475 480  
 Cys Ala Ser Gly Ser Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln  
 485 490 495  
 Cys Leu

<210> 15  
 <211> 497  
 <212> PRT  
 <213> Trichoderma reesei

<400> 15  
 Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp  
 1 5 10 15  
 Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val  
 20 25 30  
 Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr  
 35 40 45  
 Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn  
 50 55 60  
 Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser  
 65 70 75 80  
 Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val  
 85 90 95  
 Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala  
 100 105 110  
 Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser

115	120	125	
Phe Asp Val Asp Val Ser Gln	Leu Pro Cys Gly	Leu Asn Gly Ala Leu	
130	135	140	
Tyr Phe Val Ser Met Asp Ala Asp Gly	Gly Val Ser Lys Tyr	Pro Thr	
145	150	155	160
Asn Thr Ala Gly Ala Lys	Tyr Gly Thr	Gly Tyr Cys Asp Ser Gln Cys	
165	170	175	
Pro Arg Asp Leu Lys Phe Ile Asn Gly	Gln Ala Asn Val	Glu Gly Trp	
180	185	190	
Glu Pro Ser Ser Asn Asn Ala Asn	Thr Gly Ile Gly	Gly His Gly Ser	
195	200	205	
Cys Cys Ser Glu Met Asp Ile Trp	Glu Ala Asn Ser	Ile Ser Glu Ala	
210	215	220	
Leu Thr Pro His Pro Cys Thr Thr Val	Gly Gln Glu	Ile Cys Glu Gly	
225	230	235	240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp	Asn Arg Tyr Gly	Gly Thr Cys	
245	250	255	
Asp Pro Asp Gly Cys Asp Trp Asn Pro	Tyr Arg Leu Gly	Asn Thr Ser	
260	265	270	
Phe Tyr Gly Pro Gly Ser Ser Phe	Thr Leu Asp	Thr Lys Lys Leu	
275	280	285	
Thr Val Val Thr Gln Phe Glu	Thr Ser Gly Ala Ile	Asn Arg Tyr Tyr	
290	295	300	
Val Gln Asn Gly Val Thr Phe	Gln Gln Pro Asn Ala	Glu Leu Gly Ser	
305	310	315	320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp	Tyr Cys Thr Ala	Glu Glu Ala	
325	330	335	
Glu Phe Gly Gly Ser Ser Phe Ser	Asp Lys Gly	Gly Leu Thr Gln Phe	
340	345	350	
Lys Lys Ala Thr Ser Gly Gly Met	Val Leu Val Met	Ser Leu Trp Asp	
355	360	365	
Asp Tyr Tyr Ala Asn Met Leu Trp	Leu Asp Ser	Thr Tyr Pro Thr Asn	
370	375	380	
Glu Thr Ser Ser Thr Pro Gly Ala Val	Arg Gly Ser	Cys Ser Thr Ser	
385	390	395	400
Ser Gly Val Pro Ala Gln Val Glu	Ser Gln Ser	Pro Asn Ala Lys Val	
405	410	415	
Thr Phe Ser Asn Ile Lys Phe Gly	Pro Ile Gly	Ser Thr Gly Asn Pro	
420	425	430	
Ser Gly Gly Asn Pro Pro Gly	Gly Asn Pro	Pro Gly Thr Thr Thr Thr	
435	440	445	
Arg Arg Pro Ala Thr Thr Gly Ser	Ser Pro	Gly Pro Thr Gln Ser	
450	455	460	
His Tyr Gly Gln Cys Gly Gly Ile	Gly Tyr Ser	Gly Pro Thr Val Cys	
465	470	475	480
Ala Ser Gly Thr Thr Cys Gln Val	Leu Asn Pro	Tyr Tyr Ser Gln Cys	
485	490	495	
Leu			

<210> 16  
 <211> 495  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> consensus sequence

<400> 16  
 Gln Ser Ala Cys Thr Leu Gln Thr Glu Thr His Pro Pro Leu Thr Trp  
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 Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val

20	25	30
Val Ile Asp Ala Asn Trp Arg Trp	Thr His Ala Thr Asn Ser Ser Thr	
35	40	45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr	Leu Cys Pro Asp Asn	
50	55	60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly	Ala Ala Tyr Ala Ser	
65	70	75
Thr Tyr Gly Val Thr Thr Ser Ala Asp Ser	Leu Ser Ile Gly Phe Val	
85	90	95
Thr Gln Ser Ala Gln Lys Asn Val Gly	Ala Arg Leu Tyr Leu Met Ala	
100	105	110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr	Leu Leu Gly Asn Glu Phe Ser	
115	120	125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly	Leu Asn Gly Ala Leu	
130	135	140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly	Val Ser Lys Tyr Pro Thr	
145	150	155
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly	Tyr Cys Asp Ser Gln Cys	
165	170	175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln	Ala Asn Val Glu Gly Trp	
180	185	190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly	Ile Gly Gly His Gly Ser	
195	200	205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn	Ser Ile Ser Glu Ala	
210	215	220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln	Glu Ile Cys Asp Gly	
225	230	235
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Arg	Tyr Gly Gly Thr Cys Asp	
245	250	255
Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg	Leu Gly Asn Thr Ser Phe	
260	265	270
Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr	Thr Lys Lys Leu Thr	
275	280	285
Val Val Thr Gln Phe Glu Thr Ser Gly Ala	Ile Asn Arg Tyr Tyr Val	
290	295	300
Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala	Glu Leu Gly Ser Tyr	
305	310	315
Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys	Thr Ala Glu Glu Ala Glu	
325	330	335
Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly	Gly Leu Thr Gln Phe Lys	
340	345	350
Lys Ala Thr Ser Gly Gly Met Val Leu Val Met	Ser Leu Trp Asp Asp	
355	360	365
Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr	Tyr Pro Thr Asn Glu	
370	375	380
Thr Ser Ser Thr Pro Gly Ala Val Arg Gly	Ser Cys Ser Thr Ser Ser	
385	390	395
Gly Val Pro Ala Gln Leu Glu Ser Gln	Ser Asn Ala Lys Val Val Tyr	
405	410	415
Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr	Gly Asn Pro Ser Gly	
420	425	430
Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly	Thr Thr Thr Arg Arg	
435	440	445
Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly	Pro Thr Gln Thr His Tyr	
450	455	460
Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly	Pro Thr Val Cys Ala Ser	
465	470	475
Gly Thr Thr Cys Gln Val Leu Asn Glu Tyr	Tyr Ser Gln Cys Leu	
485	490	495

<210> 17  
<211> 19

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> primer  
  
<400> 17  
atgtatcgga agttggccg 19  
  
<210> 18  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> primer  
  
<400> 18  
ttacaggcac tgagagtag 19